

Db		1	MAFNDLLKQVGGVGRFQLIQVTMVVAPLLLMASHNTLQNFTAAIPPHHCRPPANANLSKD	60
Qy		61	GGLEVWLPRDRQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGIYDNSTFPSTI	120
			: : : : : :	
Db		61	GGLEAWLPDKQGQPESCLRFTSPQWGPPFYNGTEANGTRVTEPCIDGWVDNSTFPSTI	120
Qy		121	VTEWDLVCSHRALRQLAQSLYMVGVLGAMVFGYLADRLGRRKVLIILNYLQTAVSGTCAA	180
			: : : : : :	
Db		121	VTEWNLVCSHRAFRQLAQSLYMVGVLGAMVFGYLADRLGRRKVLIILNYLQTAVSGTCAA	180
Qy		181	FAPNFPPIYCAFRLLSGMALAGISLNCMTLNVEWMPIHTRACVGTTLIGYVYSLGQFLLAGV	240
			: : : : : : : : : : : : :	
Db		181	YAPNYTVYCVFRLLSGMSLASIAINCMTLNVEWMPIHTRAYVGTTLIGYVYSLGQFLLAGI	240
Qy		241	AYAVPHWRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRDLTLRALQRVARINGKREE	300
			: : : : : :	
Db		241	AYAVPHWRHLQLLVSVPPFFIAFIYSWFFIESARWYSSSGRDLTLRALQRVARINGKQEE	300
Qy		301	GAKLSMEVLRASLQKELTMKGQASAMELLRCPTLRHLFLCLSMLWFATSFAYYGLVMDL	360
			: : : : : :	
Db		301	GAKLSIEVLRRTSLQKELTLSKGQASAMELLRCPTLRHLFLCLSMLWFATSFAYYGLVMDL	360
Qy		361	QGFVGSIIYLIVIFGAVDLPKLVGFLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS	420
			: : : : : :	
Db		361	QGFVGSMYLIVIFGAVDLPKFVCFLVINSMGRRPAQMASLLLAGICILVNGIIPKSHT	420
Qy		421	IVRTSLAVLGKGCLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE	480
			: : : : : :	
Db		421	IIRTSLAVLGKGCLASSFNCIFLYTGELYPTVIRQTGLMGSTMARVGSIVSPLVSMTAE	480
Qy		481	LYPSPMLFIYGAVPVVAASAVTVLLPETLGQPLPDTVQDLESR-KGKQTRQQEHEQKYMVP	539
			: : : : : :	
Db		481	FYPSPMLFIFGAVPVVASAVTALLPETLGQPLPDTVQDLKSRSGKQNKQEQQEQKQMMP	540
Qy		540	LQASAQEKNGL 550	
Db		541	LQASTQEKNGL 551	

Sequence Comparison A

RESULT 6

035956

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ID O35956 PRELIMINARY; PRT: 551 AA.
AC O35956;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Renal organic anion transport protein 1.
GN SLC22A6 OR ROAT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=KIDNEY;
RX MEDLINE=98043701; PubMed=9374486;
RA Sweet D.H., Wolff N.A., Pritchard J.B.;
RT "Expression cloning and characterization of ROAT1. The basolateral
RT organic anion transporter in rat kidney.";
RL J. Biol. Chem. 272:30088-30095(1997).
RN [2]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
RX MEDLINE=97373539; PubMed=9228014;
RA Sekine T., Watanabe N., Hosoyamada M., Kanai Y., Endou H.;
RT "Expression cloning and characterization of a novel multispecific
RT organic anion transporter.";
RL J. Biol. Chem. 272:18526-18529(1997).
CC -!- FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC
CC ANIONS SUCH AS CYCLIC NUCLEOTIDES, PROSTAGLANDIN E2 AND URIC ACID.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL
CC MEMBRANE (POTENTIAL).
CC -!- TISSUE SPECIFICITY: STRONG EXPRESSION IN KIDNEY. VERY WEAK
CC EXPRESSION IN BRAIN. NOT DETECTED IN HEART, LUNG, LIVER, SPLEEN
CC SKELETAL MUSCLE, SMALL INTESTINE, LARGE INTESTINE, EYE OR TESTIS.
CC EXPRESSED IN THE PROXIMAL TUBULE IN THE KIDNEY.
CC -!- PTM: GLYCOSYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS.
DR EMBL; AF008221; AAC18772.1; -.
DR EMBL; AB004559; BAA22086.1; -.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR004749; Orgcat_transp.
DR InterPro; IPR005828; Sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR TIGRFAMS; TIGR00898; 2A0119; 1.
DR PROSITE; PS50850; MFS; 1.
KW Transmembrane; Transport; Glycoprotein; Ion transport.
FT TRANSMEM 136 156 POTENTIAL.
FT TRANSMEM 196 216 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT TRANSMEM 338 358 POTENTIAL.
FT TRANSMEM 396 416 POTENTIAL.
FT TRANSMEM 485 505 POTENTIAL.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 551 AA; 60766 MW; 8BA47BE628324BF2 CRC64;

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Query Match 89.5%; Score 2549.5; DB 11; Length 551;
Best Local Similarity 87.8%; Pred. No. 1.5e-203;
Matches 484; Conservative 35; Mismatches 31; Indels 1; Gaps 1;

Qy 1 MAFNDLLQQVGGVGRFQQIQVTLVLP LLLMASHNTLQNFTAAIPTHHCRPPADANLSKN 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :